



SEQUENCE LISTING

<110> Li, Yi
<120> Human G-Protein Chemokine Receptor HSATU68
<130> PF218PCT.US
<140> 09/101,518
<141> 1998-12-21
<150> PCT/US96/00499
<151> 1996-01-11
<160> 9
<170> PatentIn Ver. 2.1
<210> 1
<211> 1876
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (173)..(1420)
<400> 1
cctgaaggga gagcagggag agagaggaca gtggccagag agggctcttg gcactggagg 60
gacgctcttc ttctgcca ggggtccctg ggccgatggg atcacgcaga agaatgcgag 120
agaagcagcc ttgagaagg gaagtacta tcccagagcc cagactgagc gg atg gag 178
Met Glu
1
ttg agg aag tac ggc cct gga aga ctg gcg ggg aca gtt ata gga gga 226
Leu Arg Lys Tyr Gly Pro Gly Arg Leu Ala Gly Thr Val Ile Gly Gly
5 10 15
gct gct cag agt aaa tca cag act aaa tca gac tca atc aca aaa gag 274
Ala Ala Gln Ser Lys Ser Gln Thr Lys Ser Asp Ser Ile Thr Lys Glu
20 25 30
ttc ctg cca ggc ctt tac aca gcc cct tcc tcc ccg ttc ccg ccc tca 322
Phe Leu Pro Gly Leu Tyr Thr Ala Pro Ser Ser Pro Phe Pro Pro Ser
35 40 45 50
cag gtg agt gac cac caa gtg cta aat gac gcc gag gtt gcc gcc ctc 370
Gln Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val Ala Ala Leu
55 60 65
ctg gag aac ttc agc tct tcc tat gac tat gga gaa aac gag agt gac 418
Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn Glu Ser Asp
70 75 80
tcg tgc tgt acc tcc ccg ccc tgc cca cag gac ttc agc ctg aac ttc 466
Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser Leu Asn Phe

85										90										95										
gac	cgg	gcc	ttc	ctg	cca	gcc	ctc	aac	agc	ctc	ctc	ttt	ctg	ctg	ggg	514														
Asp	Arg	Ala	Phe	Leu	Pro	Ala	Leu	Asn	Ser	Leu	Leu	Phe	Leu	Leu	Gly															
100					105					110																				
ctg	ctg	ggc	aac	ggc	gcg	gtg	gca	gcc	gtg	ctg	ctg	agc	cgg	cgg	aca	562														
Leu	Leu	Gly	Asn	Gly	Ala	Val	Ala	Ala	Val	Leu	Leu	Ser	Arg	Arg	Thr															
115					120					125					130															
gcc	ctg	agc	agc	acc	gac	acc	ttc	ctg	ctc	cac	cta	gct	gta	gca	gac	610														
Ala	Leu	Ser	Ser	Thr	Asp	Thr	Phe	Leu	Leu	His	Leu	Ala	Val	Ala	Asp															
135					140					145																				
acg	ctg	ctg	gtg	ctg	aca	ctg	ccg	ctc	tgg	gca	gtg	gac	gct	gcc	gtc	658														
Thr	Leu	Leu	Val	Leu	Thr	Leu	Pro	Leu	Trp	Ala	Val	Asp	Ala	Ala	Val															
150					155					160																				
cag	tgg	gtc	ttt	ggc	tct	ggc	ctc	tgc	aaa	gtg	gca	ggt	gcc	ctc	ttc	706														
Gln	Trp	Val	Phe	Gly	Ser	Gly	Leu	Cys	Lys	Val	Ala	Gly	Ala	Leu	Phe															
165					170					175																				
aac	atc	aac	ttc	tac	gca	gga	gcc	ctc	ctg	ctg	gcc	tgc	atc	agc	ttt	754														
Asn	Ile	Asn	Phe	Tyr	Ala	Gly	Ala	Leu	Leu	Leu	Ala	Cys	Ile	Ser	Phe															
180					185					190																				
gac	cgc	tac	ctg	aac	ata	gtt	cat	gcc	acc	cag	ctc	tac	cgc	cgg	ggg	802														
Asp	Arg	Tyr	Leu	Asn	Ile	Val	His	Ala	Thr	Gln	Leu	Tyr	Arg	Arg	Gly															
195					200					205					210															
ccc	ccg	gcc	cgc	gtg	acc	ctc	acc	tgc	ctg	gct	gtc	tgg	ggg	ctc	tgc	850														
Pro	Pro	Ala	Arg	Val	Thr	Leu	Thr	Cys	Leu	Ala	Val	Trp	Gly	Leu	Cys															
215					220					225																				
ctg	ctt	ttc	gcc	ctc	cca	gac	ttc	atc	ttc	ctg	tcg	gcc	cac	cac	gac	898														
Leu	Leu	Phe	Ala	Leu	Pro	Asp	Phe	Ile	Phe	Leu	Ser	Ala	His	His	Asp															
230					235					240																				
gag	cgc	ctc	aac	gcc	acc	cac	tgc	caa	tac	aac	ttc	cca	cag	gtg	ggc	946														
Glu	Arg	Leu	Asn	Ala	Thr	His	Cys	Gln	Tyr	Asn	Phe	Pro	Gln	Val	Gly															
245					250					255																				
cgc	acg	gct	ctg	cgg	gtg	ctg	cag	ctg	gtg	gct	ggc	ttt	ctg	ctg	ccc	994														
Arg	Thr	Ala	Leu	Arg	Val	Leu	Gln	Leu	Val	Ala	Gly	Phe	Leu	Leu	Pro															
260					265					270																				
ctg	ctg	gtc	atg	gcc	tac	tgc	tat	gcc	cac	atc	ctg	gcc	gtg	ctg	ctg	1042														
Leu	Leu	Val	Met	Ala	Tyr	Cys	Tyr	Ala	His	Ile	Leu	Ala	Val	Leu	Leu															
275					280					285					290															
gtt	tcc	agg	ggc	cag	cgg	cgc	ctg	cgg	gcc	atg	cgg	ctg	gtg	gtg	gtg	1090														
Val	Ser	Arg	Gly	Gln	Arg	Arg	Leu	Arg	Ala	Met	Arg	Leu	Val	Val	Val															
295					300					305																				
gtc	gtg	gtg	gcc	ttt	gcc	ctc	tgc	tgg	acc	ccc	tat	cac	ctg	gtg	gtg	1138														
Val	Val	Val	Ala	Phe	Ala	Leu	Cys	Trp	Thr	Pro	Tyr	His	Leu	Val	Val															
310					315					320																				

ctg gtg gac atc ctc atg gac ctg ggc gct ttg gcc cgc aac tgt ggc 1186
 Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg Asn Cys Gly
 325 330 335
 cga gaa agc agg gta gac gtg gcc aag tct gtc acc tca ggc ctg ggc 1234
 Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser Gly Leu Gly
 340 345 350
 tac atg cac tgc tgc ctc aac ccg ctg ctc tat gcc ttt gta ggg gtc 1282
 Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe Val Gly Val
 355 360 365 370
 aag ttc cgg gag cgg atg tgg atg ctg ctc ttg cgc ctg ggc tgc ccc 1330
 Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu Gly Cys Pro
 375 380 385
 aac cag aga ggg ctc cag agg cag cca tct tct tcc cgc cgg gat tca 1378
 Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg Arg Asp Ser
 390 395 400
 tcc tgg tct gag acc tca gag gcc tcc tct tct ggc ttg tga 1420
 Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu
 405 410 415
 ggccggaatc cgggctcccc ttctgcccac agtctgactt cccgcattc caggctcctc 1480
 cctccctctg ccggctctgg ctctcccaa tctctcgct cccgggactc actggcagcc 1540
 ccagcaccac caggtctccc gggaagccac cctcccagct ctgaggactg caccattgct 1600
 gctccttagc tgccaagccc catcctgccg cccgaggtgg ctgcctggag cccactgcc 1660
 cttctcattt ggaaactaaa acttcatctt ccccaagtgc ggggagtaca aggcattggcg 1720
 tagagggtgc tgcccatga agccacagcc caggcctcca gctcagcagt gactgtggcc 1780
 atggtcccca agacctctat atttggtctt ttatttttat gtctaaaatc ctgcttaaaa 1840
 cttttcaata aacaagatcg tcaggaaaaa aaaaaa 1876

<210> 2
 <211> 415
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Glu Leu Arg Lys Tyr Gly Pro Gly Arg Leu Ala Gly Thr Val Ile
 1 5 10 15
 Gly Gly Ala Ala Gln Ser Lys Ser Gln Thr Lys Ser Asp Ser Ile Thr
 20 25 30
 Lys Glu Phe Leu Pro Gly Leu Tyr Thr Ala Pro Ser Ser Pro Phe Pro
 35 40 45
 Pro Ser Gln Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val Ala
 50 55 60
 Ala Leu Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn Glu
 65 70 75 80
 Ser Asp Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser Leu

										85			90			95		
Asn	Phe	Asp	Arg	Ala	Phe	Leu	Pro	Ala	Leu	Asn	Ser	Leu	Leu	Phe	Leu			
				100					105					110				
Leu	Gly	Leu	Leu	Gly	Asn	Gly	Ala	Val	Ala	Ala	Val	Leu	Leu	Ser	Arg			
				115					120					125				
Arg	Thr	Ala	Leu	Ser	Ser	Thr	Asp	Thr	Phe	Leu	Leu	His	Leu	Ala	Val			
				130					135					140				
Ala	Asp	Thr	Leu	Leu	Val	Leu	Thr	Leu	Pro	Leu	Trp	Ala	Val	Asp	Ala			
				145					150					155				
Ala	Val	Gln	Trp	Val	Phe	Gly	Ser	Gly	Leu	Cys	Lys	Val	Ala	Gly	Ala			
				165					170					175				
Leu	Phe	Asn	Ile	Asn	Phe	Tyr	Ala	Gly	Ala	Leu	Leu	Leu	Ala	Cys	Ile			
				180					185					190				
Ser	Phe	Asp	Arg	Tyr	Leu	Asn	Ile	Val	His	Ala	Thr	Gln	Leu	Tyr	Arg			
				195					200					205				
Arg	Gly	Pro	Pro	Ala	Arg	Val	Thr	Leu	Thr	Cys	Leu	Ala	Val	Trp	Gly			
				210					215					220				
Leu	Cys	Leu	Leu	Phe	Ala	Leu	Pro	Asp	Phe	Ile	Phe	Leu	Ser	Ala	His			
				225					230					235				
His	Asp	Glu	Arg	Leu	Asn	Ala	Thr	His	Cys	Gln	Tyr	Asn	Phe	Pro	Gln			
				245					250					255				
Val	Gly	Arg	Thr	Ala	Leu	Arg	Val	Leu	Gln	Leu	Val	Ala	Gly	Phe	Leu			
				260					265					270				
Leu	Pro	Leu	Leu	Val	Met	Ala	Tyr	Cys	Tyr	Ala	His	Ile	Leu	Ala	Val			
				275					280					285				
Leu	Leu	Val	Ser	Arg	Gly	Gln	Arg	Arg	Leu	Arg	Ala	Met	Arg	Leu	Val			
				290					295					300				
Val	Val	Val	Val	Val	Ala	Phe	Ala	Leu	Cys	Trp	Thr	Pro	Tyr	His	Leu			
				305					310					315				
Val	Val	Leu	Val	Asp	Ile	Leu	Met	Asp	Leu	Gly	Ala	Leu	Ala	Arg	Asn			
				325					330					335				
Cys	Gly	Arg	Glu	Ser	Arg	Val	Asp	Val	Ala	Lys	Ser	Val	Thr	Ser	Gly			
				340					345					350				
Leu	Gly	Tyr	Met	His	Cys	Cys	Leu	Asn	Pro	Leu	Leu	Tyr	Ala	Phe	Val			
				355					360					365				
Gly	Val	Lys	Phe	Arg	Glu	Arg	Met	Trp	Met	Leu	Leu	Leu	Arg	Leu	Gly			
				370					375					380				
Cys	Pro	Asn	Gln	Arg	Gly	Leu	Gln	Arg	Gln	Pro	Ser	Ser	Ser	Arg	Arg			
				385					390					395				
Asp	Ser	Ser	Trp	Ser	Glu	Thr	Ser	Glu	Ala	Ser	Tyr	Ser	Gly	Leu				
				405					410					415				

```
<210> 3
<211> 29
<212> DNA
<213> Homo sapiens
```

```
<400> 3
cgggatcctc catggagttg aggaagtac
```

29

```
<210> 4
<211> 30
<212> DNA
<213> Homo sapiens
```

<400> 4
ggcggatccc gctcacaagc ccgagtagga 30

<210> 5
<211> 34
<212> DNA
<213> Homo sapiens

<400> 5
gtccaagctt gccacatgg agttgaggaa gtac 34

<210> 6
<211> 57
<212> DNA
<213> Homo sapiens

<400> 6
ctgctcgagt caagcgtagt ctgggacgtc gtagggtag cacaagcccg agtagga 57

<210> 7
<211> 31
<212> DNA
<213> Homo sapiens

<400> 7
cgggatccct cccatggagt tgaggaagta c 31

<210> 8
<211> 29
<212> DNA
<213> Homo sapiens

<400> 8
cgggatcccg ctcacaagcc cgagtagga 29

<210> 9
<211> 353
<212> PRT
<213> Homo sapiens

<400> 9
Glu Ser Asp Ser Phe Glu Asp Phe Trp Lys Gly Glu Asp Leu Ser Asn
1 5 10 15

Tyr Ser Tyr Ser Ser Thr Leu Pro Pro Phe Leu Leu Asp Ala Ala Pro
20 25 30

Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys Tyr Phe Val Val Ile Ile
35 40 45

Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val Met
50 55 60

Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val Tyr
 65 70 75 80
 Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu Pro
 85 90 95
 Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe Leu
 100 105 110
 Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile
 115 120 125
 Leu Leu Leu Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val His
 130 135 140
 Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr Leu Val Lys Phe Ile Cys
 145 150 155 160
 Leu Ser Ile Trp Gly Leu Ser Leu Leu Ala Leu Pro Val Leu Leu
 165 170 175
 Phe Arg Arg Thr Val Tyr Ser Ser Asn Val Ser Pro Ala Cys Tyr Glu
 180 185 190
 Asp Met Gly Asn Asn Thr Ala Asn Trp Arg Met Leu Leu Arg Ile Leu
 195 200 205
 Pro Gln Ser Phe Gly Phe Ile Val Pro Leu Leu Ile Met Leu Phe Cys
 210 215 220
 Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln Lys
 225 230 235 240
 His Arg Ala Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu
 245 250 255
 Cys Trp Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg
 260 265 270
 Thr Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn His Ile Asp Arg
 275 280 285
 Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile Leu His Ser Cys Leu Asn
 290 295 300
 Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys Phe Arg His Gly Leu Leu
 305 310 315 320
 Lys Ile Leu Ala Ile His Gly Leu Ile Ser Lys Asp Ser Leu Pro Lys
 325 330 335
 Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly His Thr Ser Thr
 340 345 350
 Thr